

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 26, 2004, 14:48:54 ; Search time 23 Seconds

(without alignments)

2062.794 Million cell updates/sec

Title: US-10-063-579-70

Perfect score: 4791

Sequence: 1 MGLPRGFVFLVCLHQSN LVLVIGSVTVNFIILSTTI 919

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents AA.*

1: /cggn2_6/prodata/2/iaa/5A_COMB.pep:*

2: /cggn2_6/prodata/2/iaa/5B_COMB.pep:*

3: /cggn2_6/prodata/2/iaa/6A_COMB.pep:*

4: /cggn2_6/prodata/2/iaa/6B_COMB.pep:*

5: /cggn2_6/prodata/2/iaa/PCFTUS_COMB.pep:*

6: /cggn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4760	99.4	917	4 US-09-049-698-41	Sequence 41, App1
2	2879.5	60.1	914	4 US-09-193-562D-28	Sequence 28, App1
3	2879.5	60.1	914	4 US-09-223-624-6	Sequence 6, App1
4	2681	56.0	913	4 US-09-623-624-2	Sequence 2, App1
5	2431.5	50.8	903	4 US-09-113-562D-46	Sequence 46, App1
6	2426.5	50.6	903	4 US-09-223-624-18	Sequence 18, App1
7	2338.5	48.8	905	4 US-09-193-562D-2	Sequence 2, App1
8	2278	47.5	902	4 US-09-193-562D-34	Sequence 34, App1
9	2176.5	45.4	1000	4 US-09-193-562D-30	Sequence 30, App1
10	2103.5	43.9	795	4 US-09-193-562D-11	Sequence 11, App1
11	2103.5	43.9	821	4 US-09-193-562D-12	Sequence 12, App1
12	1950.5	40.7	943	4 US-09-633-59-161	Sequence 161, App1
13	1950.5	40.7	943	4 US-09-480-880A-161	Sequence 161, App1
14	1950.5	40.7	943	4 US-09-542-65A-161	Sequence 161, App1
15	1950.5	40.7	943	4 US-19-606-422B-161	Sequence 161, App1
16	1950.5	40.7	943	4 US-09-623-624-4	Sequence 4, App1
17	1950.5	40.7	943	4 US-09-221-107-161	Sequence 161, App1
18	1950	40.7	920	4 US-09-633-597-357	Sequence 357, App1
19	1948.5	40.7	943	4 US-09-193-562D-32	Sequence 32, App1
20	1913	39.9	942	4 US-09-919-172-87	Sequence 87, App1
21	1706	35.6	791	4 US-09-643-597-170	Sequence 170, App1
22	1705	35.6	791	4 US-09-488A-170	Sequence 170, App1
23	1705	35.6	791	4 US-09-542-615A-170	Sequence 170, App1
24	1705	35.6	791	4 US-09-606-421B-170	Sequence 170, App1
25	1275	26.6	592	4 US-09-64-597-169	Sequence 169, App1
26	1275	26.6	592	4 US-09-480-884A-169	Sequence 169, App1
27	1275	26.6	592	4 US-09-542-615A-169	Sequence 169, App1

ALIGNMENTS

28	1275	26.6	592	4 US-09-606-421B-169	Sequence 169, App1
29	987.5	20.6	342	4 US-09-193-562D-13	Sequence 13, App1
30	693.5	14.5	228	4 US-08-649-667-9	Sequence 9, App1
31	693.5	14.5	228	4 US-09-224-110-9	Sequence 9, App1
32	693.5	14.5	228	5 PCT-US95-07289-9	Sequence 9, App1
33	468	9.8	203	4 US-09-193-562D-3	Sequence 45, App1
34	218	4.6	40	4 US-09-049-698-43	Sequence 3, App1
35	174.5	3.6	1541	3 US-08-296-791-3	Sequence 3, App1
36	174.5	3.6	1541	4 US-09-839-996-3	Sequence 3, App1
37	174.5	3.6	1541	4 US-10-080-505-3	Sequence 3, App1
38	174.5	3.6	1541	5 PCT-US95-10661A-3	Sequence 3, App1
39	167	3.5	31	4 US-09-049-698-43	Sequence 43, App1
40	157.5	3.3	1702	4 US-08-39-996-5	Sequence 5, App1
41	157.5	3.3	1702	4 US-10-080-505-5	Sequence 5, App1
42	157.5	3.3	1702	4 US-10-080-505-5	Sequence 5, App1
43	157.5	3.2	1612	1 US-08-169-927-2	Sequence 2, App1
44	151	3.2	1426	3 US-09-136-574A-43	Sequence 43, App1

RESULT 1					
US-09-049-698-41					
; Sequence 41, Application US/09049698					
; Patent No. 6388792					
GENERAL INFORMATION:					
; APPLICANT: BILLING-MEDELL, PATRICIA A.					
; APPLICANT: COHEN, MAURICE					
; APPLICANT: COPITITS, TRACEY L.					
; APPLICANT: FREDMAN, PAULIA N.					
; APPLICANT: HADDEN, MARK					
; APPLICANT: KLAAS, MICHAEL R.					
; APPLICANT: ROBERTS-RAPP, LISA					
; APPLICANT: RUSSELL, JOHN C.					
; APPLICANT: STROUPE, STEPHEN D.					
TITLE OF INVENTION: REAGENTS AND METHODS FOR THE					
TITLE OF INVENTION: USESEQ FOR DETECTING DISEASES OF THE GASTROINTESTINAL					
TITLE OF INVENTION: TRACT					
NUMBER OF SEQUENCES: 51					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Abbott Laboratories					
STREET: 100 Abbott Park Road					
CITY: Abbott Park					
STATE: IL					
COUNTRY: USA					
ZIP: 60064-3500					
COMPUTER READABLE FORM:					
; MEDIUM TYPE: Diskette					
; COMPUTER: IBM Compatible					
; OPERATING SYSTEM: DOS					
; SOFTWARE: FASTSEQ DATA FOR Windows Version 2.0					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/09/049,698					
; CLASSIFICATION:					
; PRIORITY APPLICATION DATA:					
; APPLICATION NUMBER: 08/828,856					
; FILING DATE: 31-MAR-1997					
; ATTORNEY/AGENT: INFORMATION:					
; NAME: Becker, Cheryl L.					
; REGISTRATION NUMBER: 35,441					
; REFERENCE/DOCKET NUMBER: 6068.US.P1					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: 847/935-1729					
; TELEFAX: 847/938-2623					
; INFORMATION FOR SEQ ID NO: 41:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 917 amino acids					
; TYPE: amino acid					
; STRANDEDNESS: single					

: TOPOLOGY: linear
 : MOLECULE TYPE: No. 6368792e
 : US-09-049-698-41

Query Match 99.4%; Score 4760; DB 4; Length 917;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 916; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 MGLFRGFVFLIVLCLHQNSNTSFKLINNGNEDIVIDPSVPEDEKEISEQIDEMVTAS 60
 Db 1 MGLFRGFVFLIVLCLHQNSNTSFKLINNGNEDIVIDPSVPEDEKEISEQIDEMVTAS 60

Qy 61 TYLFEATEKREFFKNTVSILITENWKENPQYKRPKHENHADIVTAPPTPGRDEPYTQ 120
 Db 61 TYLFEATEKREFFKNTVSILITENWKENPQYKRPKHENHADIVTAPPTPGRDEPYTQ 120

Qy 121 FTECGERGEKEYHTFPDILLGKQKNEYGPQGKLFYHEWAHLRGYDNEYNDQPFYRAKS 180
 Db 121 FTECGERGEKEYHTFPDILLGKQKNEYGPQGKLFYHEWAHLRGYDNEYNDQPFYRAKS 180

Qy 181 KIBATRCSAGISGRNRVYKCQGGSCSLRACRIDSSTKLYGKDCQFFPKYOTEKASIMPM 240
 Db 181 KIBATRCSAGISGRNRVYKCQGGSCSLRACRIDSSTKLYGKDCQFFPKYOTEKASIMPM 240

Qy 241 QSDSVVBFNEKTHOBAPSQNICKNFRSTWEVINSSEDFKNTPMVTPPPPFVFSL 300
 Db 241 QSDSVVBFNEKTHOBAPSQNICKNFRSTWEVINSSEDFKNTPMVTPPPPFVFSL 300

Qy 301 KISQRIVCLVLDLRSMSMGKDRLNRAKQAAKHFLLQTVENGWSWGMVHPFSTATIVNKJ 360
 Db 301 KISQRIVCLVLDLRSMSMGKDRLNRAKQAAKHFLLQTVENGWSWGMVHPFSTATIVNKJ 360

Qy 361 QIKSSDENTMAGLPTPLGGTSICSGKIAFQVIGELHSQDGSEVLLTDGEDNTAS 420
 Db 361 QIKSSDENTMAGLPTPLGGTSICSGKIAFQVIGELHSQDGSEVLLTDGEDNTAS 420

Qy 421 SCIDEVKSGATVHFAIGRAADEAVTEMSTKGGSHFYVSDEAQNGLDAFGALTSGN 480
 Db 421 SCIDEVKSGATVHFAIGRAADEAVTEMSTKGGSHFYVSDEAQNGLDAFGALTSGN 480

Qy 481 TDLSOKSPOSEKGLTNSNAMNDTVIDSTVGDTFELTNSLUPPSISLWDPSGTIM 540
 Db 481 TDLSOKSPOSEKGLTNSNAMNDTVIDSTVGDTFELTNSLUPPSISLWDPSGTIM 540

Qy 541 ENFTVDAISKMAYLSPPTAKTGTVWNLQAKANPETLTITYTSRANNSYPITNAKM 600
 Db 541 ENFTVDAISKMAYLSPPTAKTGTVWNLQAKANPETLTITYTSRANNSYPITNAKM 600

Qy 601 NDVNSFSPSPMIYAEIILQGYVPLGANTTAFLESQNHTEVIELLDNGAGDSFNDGV 660
 Db 601 NDVNSFSPSPMIYAEIILQGYVPLGANTTAFLESQNHTEVIELLDNGAGDSFNDGV 660

Qy 661 YSRFTATENGRSLSKVRHGGANTARLKRPLNRAAYIPGWVNGEIEANPREFID 720
 Db 661 YSRFTATENGRSLSKVRHGGANTARLKRPLNRAAYIPGWVNGEIEANPREFID 720

Qy 721 EDTQTTLEDPSRTASGGAVPSQYPSLPLDQYPPSQTLDTDAVHEKDILTWAGDN 780
 Db 721 EDTQTTLEDPSRTASGGAVPSQYPSLPLDQYPPSQTLDTDAVHEKDILTWAGDN 780

Qy 781 FDVGKVQYRIRIASILDLRSDDALONTNTDLSPEAKNSKESPKPENISEBATH 840
 Db 781 FDVGKVQYRIRIASILDLRSDDALONTNTDLSPEAKNSKESPKPENISEBATH 840

Qy 841 IFIAKSIDKSNTSKVSNIAQVTLFIPQANPDDIDPPTPTPKSHNSGNTSTL 900
 Db 841 IFIAKSIDKSNTSKVSNIAQVTLFIPQANPDDIDPPTPTPKSHNSGNTSTL 900

Qy 901 VLSVGSVVNFILSTI 919
 Db 901 VLSVGSVVNFILSTI 919

Qy 841 IFIAKSIDKSNTSKVSNIAQVTLFIPQANPDDIDPPTPTPKSHNSGNTSTL 917
 Db 841 IFIAKSIDKSNTSKVSNIAQVTLFIPQANPDDIDPPTPTPKSHNSGNTSTL 917

Qy 720 D-EDQTTLDEDTSRASGGAEVSVQPSLPLDQYPPSQTLDTDAVHEDKII-LWTAP 777

RESULT 2

US-09-193-562D-28

Sequence 28, Application US/09193562D

Patent No. 6309857

GENERAL INFORMATION:
 APPLICANT: Pauli, Benedict U.
 TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium-Activating Chloride Channel-Adhesion MoleculesFILE REFERENCE: 18617 0052
 CURRENT APPLICATION NUMBER: US/09/193-562D
 PRIORITY FILING DATE: 1998-11-17
 NUMBER OF SEQ ID NOS: 47SEQ ID NO: 28
 TYPE: PRT
 ORGANISM: Homo sapiensUS-09-193-562D-28
 Query Match 60.1%; Score 2879.5; DB 4; Length 914;
 Best Local Similarity 61.6%; Pred. No. 8.3e-248;
 Matches 563; Conservative 124; Mismatches 216; Indels 11; Gaps 8;Qy 1 MGHLFRGFVFLIVLCLHQNSNTSFKLINNGNEDIVIDPSVPEDEKEISEQIDEMVTAS 60
 Db 1 MGHLFRGFVFLIVLCLHQNSNTSFKLINNGNEDIVIDPSVPEDEKEISEQIDEMVTAS 60
 Qy 1 MGPKKSSVEILLHLIGALSMSLIQUNNNNGEGIVIAIDPNVPEETLIOIQKDMVTOA 60
 Db 1 MGPKKSSVEILLHLIGALSMSLIQUNNNNGEGIVIAIDPNVPEETLIOIQKDMVTOA 60Qy 60 STYLEATEKRFPEKNTSILIPENWNENPOYKRPKHENHADIVIYAPPTLPGRDPYTK 119
 Db 61 SLYLFEAETKRFPEKNTSILIPENWNENPOYKRPKHENHADIVIYAPPTLPGRDPYTK 119
 Db 61 SLYLFEAETKRFPEKNTSILIPENWNENPOYKRPKHENHADIVIYAPPTLPGRDPYTK 120Qy 120 QFTECGEKEYHTFPDILLGKQKNEYGPQGKLFYHEWAHLRGYDNEYNDQPFYRAKS 179
 Db 121 QMNGCEKGERIHTLPDIAGCKLAELYGPQGRAFVHEWAHLRGYDNEYNDQPFYRAKS 180Qy 180 KKEATRCSAGISGRNRVYKCQGQSCSLSACRIDSSTKLYGKDCQFPDKYOTEKASIMF 239
 Db 181 -RQAVRCSAGITNVYKKCQGQSCYTKRCDFNKTYGLYERGCFVLSQROTERAKSIMF 239Qy 240 MQSISDVVEFCNEETHNCAPSTQNLKCNFRSTWEVINSSEDFKNTPMVTPPPPFVFSL 299
 Db 240 AQHDSIVECTEONHNKEAPNQKONLRLSTWEIRDSEFKKTPMTIQPNPZTFSL 299Qy 300 LKISRIVCLVLDKGSMGKDRLNRMNOAKHFLQTVENGWSWGMVHFSTATIVNKL 359
 Db 300 LQIGRIVCLVLDKGSMGATGNRLNQAGFLQTVENGWSWGMVHFSTATIVNKL 359Qy 360 IQLKSSDERTMLAGLPTPLGGTSICSGKIAFQVIGELHSQDGSEVLLTDGBDNTA 419
 Db 360 IQLINSDRDTLAKRLPAALASGGTSICSLRSATVIRKLY-DTGSISIVLTDGEDNTI 418Qy 420 SSCIDEVKSGATVHFAIGRAADEAVTEMSTKGGSHFYVSDEAQNGLDAFGALTSG 479
 Db 420 NGAVSORSTQLESKGTLQSONGTVIYDSTVKGKDTFLFLTVTQPOQILWDPQSKQ 478Qy 480 NTDLGKSLOLESKGTLTNSNAMNDTVIDSTVGDTFELTNSLUPPSISLWDPSGTI 539
 Db 479 MNKDYNSFSPSPMIYAEIILQGYVPLGANTTAFLESQNHTEVIELLDNGAGDSFNDGV 538Qy 540 MENFTDATSKMAYLSPPTAKTGTVWNLQAKANPETLTITYTSRANSSVPITVNAK 599
 Db 541 QGGFIVDNTKNAIQIOPGIAKVGTWKLQASS-QMILTVTSRANATLPPITVTSK 596Qy 600 VYSRIFTAYENGRISSLKVRHGGNTANLKLRLPMLNRAAYIPGWVNGEIEANPFRPFI 719
 Db 600 MNKDYNSFSPSPMIYAEIILQGYVPLGANTTAFLESQNHTEVIELLDNGAGDSFNDGV 659

Qy 597 TNKDTSKFPPSPLVVANIROGASPLRASVTLIESVNGKTVTQIQLDNGAGADATXDDG 656

Qy 660 VYSRIFTAYENGRISSLKVRHGGNTANLKLRLPMLNRAAYIPGWVNGEIEANPFRPFI 719
 Db 667 VYSRIFTAYDINGRSVKAERRVIPQSGALYIPWIENDBIQNWPRPFI 716

Qy 720 D-EDQTTLDEDTSRASGGAEVSVQPSLPLDQYPPSQTLDTDAVHEDKII-LWTAP 777

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Om protein - protein search, using SW model

Run on: April 26, 2004, 14:43:13 ; Search time 50 Seconds
(without alignments)

5799.225 Million cell updates/sec

Title: US-10-063-579-70

Perfect score: 4791

Sequence: MGLFRGFVFLVLCLLHQSN.....LVLSVIGSVVIVNFILESTI 919

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	4763	99.4	917	Q9UNF7 homo sapien
2	2884.5	60.2	914	Q9UPC6 homo sapien
3	2882.5	60.2	914	Q95151 homo sapien
4	2879.5	60.1	914	Q9UNF6 homo sapien
5	2765	57.7	917	Q9TUB5 sus scrofa
6	2681	56.0	913	Q9D726 mus musculus
7	2677	55.9	913	Q8R049 mus musculus
8	2396	50.0	469	Q9NXP1 homo sapien
9	2343.5	48.9	909	Q91ZFS mus musculus
10	2343.4	48.9	902	Q9EOR4 mus musculus
11	2341.5	48.9	905	Q18741 bos taurus
12	2333	48.7	902	Q9R070 mus musculus
13	2332	48.7	902	Q9QX15 mus musculus
14	2331	48.7	902	Q8C324 mus musculus
15	2324	48.5	902	Q8CCM1 mus musculus
16	2319.5	48.4	901	Q88860 mus musculus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	4763	99.4	917	Q9UNF7 homo sapien
2	2884.5	60.2	914	Q9UPC6 homo sapien
3	2882.5	60.2	914	Q95151 homo sapien
4	2879.5	60.1	914	Q9UNF6 homo sapien
5	2765	57.7	917	Q9TUB5 sus scrofa
6	2681	56.0	913	Q9D726 mus musculus
7	2677	55.9	913	Q8R049 mus musculus
8	2396	50.0	469	Q9NXP1 homo sapien
9	2343.5	48.9	909	Q91ZFS mus musculus
10	2343.4	48.9	902	Q9EOR4 mus musculus
11	2341.5	48.9	905	Q18741 bos taurus
12	2333	48.7	902	Q9R070 mus musculus
13	2332	48.7	902	Q9QX15 mus musculus
14	2331	48.7	902	Q8C324 mus musculus
15	2324	48.5	902	Q8CCM1 mus musculus
16	2319.5	48.4	901	Q88860 mus musculus

Query Match Score 4763; DB 4; Length 917;
Best Local Similarity 99.4%; Pred. No. 2.1e-295;
Matches 916; Conservative 0; Mismatches 1;
Indels 2; Gaps 1;

QY 1 MGIFRGFVLLVCLLHQNSNTFILNNNGEDIVIDPSVPDEKEIIEQDNWTTAS 60

Db	1	MGLFRGFVFLVLCLLHQSNSTFILKNNNGFEDIVIDPSVPEDEKTEQFEDMTTAS	60	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; OS
QY	61	TYLFEATEREFFFKVNSVIIIPENKPNPKRPHENKRHADIVIAPTLGRDEPTTKQ	120	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9601;
Db	61	TYLFEATEREFFFKVNSVIIIPENKPNPKRPHENKRHADIVIAPTLGRDEPTTKQ	120	RN RP SEQUENCE FROM N.A. [1]
QY	121	FTECEKGFIYHFEDLIGKQKBYGPCKLFYTHEWHLRGVFDENEQDFYRAKS	180	RX MBDLINE=904056; PubMed=9828122; Gruber A.D., Eible R.C., Ji H.L., Schreur K.D., Fuller C.M., Pauli B.U.; RT Genomic cloning, molecular characterization, and functional analysis of human CLCA1, the first human member of the family of Ca2+-activated Cl- channel proteins." RA PA
Db	121	FTECEKGFIYHFEDLIGKQKBYGPCKLFYTHEWHLRGVFDENEQDFYRAKS	180	RT of human CLCA1, the first human member of the family of Ca2+-activated Cl- channel proteins." RL
QY	181	KIEATRCAGISGARNVYKQGGCSLSRACRIDSTKLGYKDCQFPDKVQEKA SIMEM	240	DR AAC55429; 1. -
Db	181	KIEATRCAGISGARNVYKQGGCSLSRACRIDSTKLGYKDCQFPDKVQEKA SIMEM	240	DR GO; GO:0016021; C: integral-gated chloride channel activity; IEA.
QY	241	QSIDVVVFENKEKNEQEATSLQNRKCNFSTWIEISNEBDFNTIPVTPPPPVISL	300	DR GO; GO:0005247; P: voltage-gated chloride channel activity; IEA.
Db	241	QSIDVVVFENKEKNEQEATSLQNRKCNFSTWIEISNEBDFNTIPVTPPPPVISL	300	DR GO; GO:0006821; P: chloride transport; IEA.
QY	301	KISORIVCLVLDKSGSMGKDRLLRMNOAAKHFLLQTENGSSWGMVHDFSTATIVNL	360	DR InterPro; IPR00131; ATPase Gamma.
Db	301	KISORIVCLVLDKSGSMGKDRLLRMNOAAKHFLLQTENGSSWGMVHDFSTATIVNL	360	DR InterPro; IPR004727; CacC_Prot1.
QY	361	QIKSSDERTNIMAGLPTPLGGTSTICSGKLYKAFOVIGELHSOLGDSEVLLTGDENTAS	420	DR Pfam; PF00092; vwa_1.
Db	361	QIKSSDERTNIMAGLPTPLGGTSTICSGKLYKAFOVIGELHSOLGDSEVLLTGDENTAS	420	DR SMART; SM00327; vwa_1.
QY	421	SCIDEVKQSGAVIHTALGRAADEAVITEMSKITGGSHFYKSDLEQNLGLIDAEGALTSGN	480	DR TIGRFAMs; TIGR00868; hcAccC; 1.
Db	421	SCIDEVKQSGAVIHTALGRAADEAVITEMSKITGGSHFYKSDLEQNLGLIDAEGALTSGN	480	DR PROSITE; PS00155; ATPase_Gamma; 1.
QY	481	TDLSQKSLQLESKGLTINSNAMWNTVVISSTVGDTPFLITNLSPPSISLWDPSGTM	540	DR PROSITE; PS05024; VWEFA; 1.
Db	481	TDLSQKSLQLESKGLTINSNAMWNTVVISSTVGDTPFLITNLSPPSISLWDPSGTM	540	DR SEQUENCE 914 AA; 10016 MN; 7761362B66752AA3 CRC64;
QY			Query Match 60.2%; Score 2884.5; DB 4; Length 914;	
Db			Best Local Similarity 61.7%; Pre. No. 2-175; Indels 11; Gaps 8; Matches 564; Conservative 124; Mismatches 215; Delins 11; Gaps 8;	
QY			QY 1 MGLFRGFVFLVLCLLHQs-NTSF1KLANNNGFEDIVIDPSVPEDEKTEQFEDMTVTA 59	
Db			Db 1 MGPFKSSVFLVLLLEGALNSLICLNQNYEGIVVAIDPNVPDETELIQQIDMVTA 60	
QY			QY 60 STYLFATEKRPFKONVSLPENKVNPOYKRPKPHENKHADIVTAPPFLGRDPEPYTK 119	
Db			Db 61 SLYLFATEKRPFKONVAILPETWTKAIDVPRKLEYTKNADVLVAESTPPGNDEPYTE 120	
QY			QY 120 QFTECGERGEYHTFPFLIGKQNTGPPERLTVFWEALLRWGQFDETNEDQFPYRAKS 179	
Db			Db 121 QMGNCGEKGERHTLPDIAGKLLAYGPQSKAFYTHEWALLRWGQFDETNNDKEYLNSG 180	
QY			QY 180 KKEATRCSAGISGRVRYKCOGGCSCLSACRIDSTKLGYKDQCFPDKVQTEKA SIMP 239	
Db			Db 181 -RQAVRSAGATGIVNVKCGGSCTYRFTNKTGFLPKGCFLVQSROTERASIMF 239	
QY			QY 240 MQSIDSVEFCNEKTHNQCEAQLNQKCNFRSTWEVTSNNSDFKNT1PMTPPPPPVSFL 299	
Db			Db 240 AQHDSTIVTEQNFHRKREAPKQNQCNURSTWEVTDSDFKKTPMTQPNNTFSL 299	
QY			QY 300 LKTSQRTIVCLVLDKSGSMGKDRLLMNOAAKHFLLQTENGSSWGMVHDFSTATIVNL 359	
Db			Db 300 LQIGRQIVCLVLDKSGSMATGNRLRNQAGOLFLLQTENGSSWGMVHDFSTATIVNL 359	
QY			QY 360 IQIKSSDERTNIMAGLPTPLGGTSTICSGKLYKAFOVIGELHSOLGDSEVLLTGDENTAS 419	
Db			Db 360 IQINNSPDTLAKELPRAASGTISGURAFTRYKRY PTDSGEIVLTDGDNTI 418	
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ID	Q9UPC6;			
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DT	01-MAY-2000 (TREMBrel. 13. Created)			
DT	01-MAY-2000 (TREMBrel. 13. Last sequence update)			
DT	01-MAY-2003 (TREMBrel. 24. Last annotation update)			
	Calcium-dependent chloride channel-1.			
	CaHClCh1.			
RESULT 2				
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DT				
DT				
DT				
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QY				

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2004, 04:46:55 ; Search time 168 Seconds

(without alignments)
 3035.714 Million cell updates/sec

Title: US-10-063-579-70

Perfect score: 4791

Sequence: 1 MGLPFGFVFLVLCLLHQSN.....LVLSWIGSVVIVNFIILSTI 919

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Pgapop 6.0 , Pgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

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-DB_ISSUED_PATENTS_NA
-QPAT=fastD
-UNITS=5its
-MATRIX=blosum62 -TRANS=human0 -CDI
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGBLOCK
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Database :

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6: /gn2_6/podata/2/ina/backfiles.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4760	99.4	3043	4	US-09-542-615A-160	Sequence 16, APP
2	4760	99.4	3181	4	US-09-542-615B-160	Sequence 18, APP
3	2882.5	60.2	3007	4	US-09-542-615D-27	Sequence 27, APP
4	2879.5	60.1	2745	4	US-09-542-624-5	Sequence 5, APP
5	2681	56.0	2931	4	US-09-542-624-1	Sequence 1, APP
6	2341.5	48.9	3317	4	US-09-542-624-1	Sequence 1, APP
7	2282	47.6	3022	4	US-09-542-624-3	Sequence 33, APP
8	2191.5	45.7	3418	4	US-09-542-624-3	Sequence 29, APP
9	1950.5	40.7	2970	4	US-09-542-624-3	Sequence 31, APP
10	1950.5	40.7	3190	4	US-09-542-624-3	Sequence 3, APP
11	1950.5	40.7	3951	4	US-09-542-643-597-160	Sequence 160, APP
12	1950.5	40.7	3951	4	US-09-480-884A-160	Sequence 160, APP

ALIGNMENTS

RESULT 1

US-09-049-698-16
 Sequence 16, Application US/09049698
 Patent No. 6388792

GENERAL INFORMATION:

APPLICANT: BILLING-MEDDEL, PATRICIA A.

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITT, TRACEY L.

APPLICANT: FRIDMAN, PAULA N.

APPLICANT: HAYDEN, MARK

APPLICANT: KLAAS, MICHAEL R.

APPLICANT: ROBERTS, LISA

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS FOR THE

USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

CITY: 100 Abbott Park Road

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,698

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,856

Db	674	AAGATGTCATTCTTCCGTATAAGTA	CAACGAAAGAACAGATTCATATGGTTATG	733
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Db	734	CAAGATTTGATTCTGTCGAAATTGTAA	CAGAAAAACCATATTCAAGCTCCA	793
QY	261	SerLeuGlnAsnLysCysAsnPheArgSerThrPheGlu	ValIleSerIleSerIleSerGlu	280
Db	794	AGCTAAACATAGTAGCATTGCAATTG	TAGACTGGGGTGTGATTAGCTTGAG	853
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Db	854	GATTAAACACATACCCATGGTACACCC	CTCCACCTGCCTCTGTTCTGATAGTC	913
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Db	914	AAGATCACTCAAGATATTGTGCTTA	GTGCTGAAACCAGGGGAAAG	973
QY	321	AspArgGluAsnArgMetAsnGlnAlaAlaLysHis	PhsLeuLengNthrValGluAsn	340
Db	974	GACCGCTTAATGCAATGAACTTCCCGCTGCGAGAC	CTGTTGAAAT	1033
QY	341	GlySerIrrpValPheGlyMetValIleAspSerThrAla	ThrValLeuValAsnLysLeuIle	360
Db	1034	GGATCTGGTGGGGGTTGTTCTACTGTATGCTA	TGCAATTGAAATAGCCTAATG	1093
QY	361	GlnIleIysSerAspGluLysArgSerThrLeuMetAla	GlyLysIrrpThrPheLeuIle	380
Db	1094	CAAAAAGCAGTGTGATGAANGAAACATCATG	GCAGATTACCTACATATCTCTG	1153
QY	381	GlyGlyIrrpSerIleCysSerGlyIleIlysIrrpAla	GlyGluGlnValIleGlyLeuLeuIle	400
Db	1154	GGGGRACATCCATCTGTCCTGAAATTATGCAATT	TCAGGTGGAGCAGCAT	1213
QY	401	SerGlnIleAspDglySerGluValLeuLeuIleThrAsp	GlyGluAsnThrAlaSer	420
Db	1214	TCCCCAACCTCGATGATGCCGAGACTCTGGT	GACTATGGGGAGGATAAACCTGGCAAGT	1273
QY	421	SerCysIleAspGluValLysGlnSerIleAlaIle	ValAlaHisPheIleAlaLeuGlyArg	440
Db	1274	TCTTGTTATGTGATGAACTGTCATTTTCA	TGTTATGCTTTGGGAGAA	1333
QY	441	AlaIleAspGluValIleGluMetIleSerGlySer	IleThrGlyGlySerHistidylVal	460
Db	1334	GCTGCTGATGAACTGAACTGATAGAGATAGC	GAGATACAGGGAACTCATTTTTGTT	1393
QY	461	SerAspGluAlaGlnAsnGlyLeuIleAspAlaIle	PheGlyAlaLeuThrSerGlyAsn	480
Db	1394	TCATGAGCTGAGCTAGAACATGGCCTATGAGCT	TTGGGCTTCTACATGGGAAAT	1453
QY	481	ThrAspIleSerIleSerIleGlnLeuGluSerIlys	GlyLeuThrLeuAsnSerAsn	500
Db	1454	ACTCATCTCCGAAACTCCCTCAAGTCAGTCGA	AAAGTAGGATTAACGTGATGAAAT	1513
QY	501	AlaIlePheAspAlaIleSerIleSerIleGlySer	IleValGlyIleAspThrPhePheLeu	520
Db	1514	GCCCGGAGAAACGACACTGCTAAATCATGAACT	ACGTCGAAAGCTCCTCTC	1573
QY	521	IleThrIrrpAsnSerLeuProSerIleSerIle	LeuIrrpAspProSerGlyThrIleMet	540
Db	1574	TTGACATGCAACGTCCTCCGAACTTCTCCTG	CGGATCCCTGGAACTTCTGGAACAT	1633
QY	541	GluAsnPheThrValAspAlaIleSerIleSerIle	MetAlaIleLeuSerIleProGlyThrIle	560
Db	1634	GAIAATTTCACAGTGATGCAACTTCCAAAATGGC	CTGATTCAGGAACTCAGGAACTGCA	1693
QY	561	LysValGlyThrIrrpAlaIleAsnProGluThrIle	LeuIrrpIleAlaAsnProGluThrIle	580
Db	1694	AAGTGGGCACTTCGCTGCAATACTTCAGGCA	AAATTCTCAGTCAGGAACTTAAATTG	1753
QY	581	ThrValThrSerGlnAlaAlaSerSerValPro	PheIleThrValAlaAlaLysMet	600
Db	1754	ACGAACTCTCTCAAGCAGCAAAATTCTCTG	GGCCCTCCAAATTCAGTCAGTCAGGAACTTAAATTG	1813

Db	265	CCTGAGAATTGGAGAAATCCTAGTACAAAAGCCAAACATGAAACATAACT	324	
Qy	101	AlaAspValIleValalaProProThrIleLeuProGlyArgAspGluPro	120	
Db	325	GCTGATTTATAGTGGACCACTACTCCAGGAGATGAACTACACCGCG	384	
Qy	121	PhePheGluCysGlyGluLysGlyGluLysGlyGluLysLeuAsnSer	140	
Db	385	TTCACAGATGCGGAGAAAGCGATCATCTACCTAACCTCTACTGAA	444	
Qy	141	LysLysGlnAsnGluLysGlyProProGlyLysLeuPheValHisGlu	160	
Db	445	AAAACAATGATGATGGACCACCGCACAACTCCACCTCTACTGAA	504	
Qy	161	ArgTrpGlyValPheAspGluGlyProProGlyLysLeuPheValHisGlu	180	
Db	505	CGTGGGAAGGTGGTTGAGTAGATAATGAAATCAGCTTACGCCCTTCA	564	
Qy	181	LysIleGluAlaThrArgCysSerAlaGlyIleSerGlyArgAsnArg	200	
Db	565	AAATCGAGCACAAAGGTGTCGGAGATCTCTGGTAAATGTTAAAGTGT	624	
Qy	201	GlnGlyGlySerCysLeuSerArgAlaCysArgIleSerGlyLeuThrGly	220	
Db	625	CAGGAGGGAGGCGTCTAGTAGATGAGCAGATTCTAACAACTGTATGA	684	
Qy	221	LysAspPCysGlnPhePheProAspLysValGlnThrGluLeuAsaSer	240	
Db	685	AAAGATTGCACTCTTCCTGTATAAATACAAACAGAAAGCATCATAGTT	744	
Qy	241	GlnSerIleAspSerValGluPheCysAsnGluLysThrHisAsnD17Glu	260	
Db	745	CAAGTGTGATTCTGTGATTCTAACAAACCCATAATCAAGCTCA	804	
Qy	261	SerLeuGlnAsnIleLysCysAspPheArgSerThrPheGluValIleSer	280	
Db	805	AGCCTACAAACAACTAACGCAATTGCAATTGAGAAGTACATGGAGT	864	
Qy	281	AspPheLysAsnThrIleProMetValThrProProProValPheSer	300	
Db	865	GATTAAACCATACCATGGTGGACCTCTCCACCTGTCTCATTTGT	924	
Qy	301	LysIleSerGlnArgIleValCysLeuValLeuAspLysSerGlySeMet	320	
Db	925	AGATCGTAAGATGTTGCTTAGTCGTTGAGATGGGGTAAAG	984	
Qy	321	AspArgLeuAsnArgMetAsnGlnAlaAlaLysIleSerGluLys	340	
Db	985	GACCGCTTAACTATGATGATTCAGGCAAACATTCTGCTGAGTCGAA	1044	
Qy	341	GlySerIlePheValHisPheAspSerThrAlaThrIleValAsnLysLeu	360	
Db	1045	GGATCTGGGGGGGTGGTCACTTGATGACTGTTGAACTATGTA	1104	
Qy	361	GlnIleLysSerAspGluArgAsnThrLeuMetAlaGlyLeuPro	380	
Db	1105	CAATAAAGCAGTGAAGAAACACTCATGGCAGGATPACCTACATCCTG	1164	
Qy	401	SerGlnIleAspGlySerGluValLeuLeuThrAspGlyGluAspAsn	420	
Db	1225	TCCCRATGCGGTTGATGAACTACGCTGACTATGCTGAACTGCA	1284	
Qy	421	SerCysIleAspGluValIleMetSerIleGlyLeuGlyLeuAsp	440	
Db	1165	GGGGAACTTCATCTCTGCTGAAATATGCTGAGAGCTCAT	1224	
Qy	441	AlaAlaAspGluValIleGluMetSerIleGlyCysIleGlySer	460	
Db	1345	GCTGCTGTGAGCAGGAAATAGGATGAGCAGGAGCTTATGTT	1404	
Qy	461	SerAspGluIleGlnAsnAsnGlyIleIleAspAlaPheGlyAlaLeuThr	480	
Db	1405	TGAGTAAAGTCGAACATGGCCTCATGATGTTGGGCTTCAATCAGGAA	1444	
Qy	481	ThrAspIleSerGlyLysSerIleGluSerIleLeuAsnSer	500	
Db	1465	ACTGATCTCTCCAGAGTCCTTGCTGCTGAAAGTAACTGAAATGAA	1524	
Qy	501	AlaTriPheAspAspThrValIleLeuAspSerIleSerIleValIleAsp	520	
Db	1525	GCCTGGAGACGACTGTCATAATGADTAGCTGGCAAAAGACACGTT	1584	
Qy	521	IleThrIlePheAspSerProSerIleLeuIlePheGlyThrIleMet	540	
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Qy	541	GluAsnPheThrValAspAlaThrSerLysSerIleLeuSerIlePheGly	560	
Db	1645	GAAATTTCACAGTGGAACTCTCCAAATGGCTATCTCGATTTCCGGAA	1704	
Qy	561	LysValGlyThrPheAlaPheAspGluIleGlnAlaLysAlaAsnPro	580	
Db	1705	AAGTGGGCACTGGCATACATCTCAAGCAGGAACTTAACTGATGAA	1764	
Qy	581	ThrValThrSerArgAlaAlaAsnSerValProProIleThrLeuThr	600	
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Qy	601	AsnLysAspValAsnSerPheProSerProMetIleValThrAlaGluIle	620	
Db	1825	ATTAAGGGCTTAACAGTTCCCAAGCCAAATGATTTTACAGAAATT	1884	
Qy	621	TyrValProValLeuGlyAlaAlaValIleValAlaPheIleGluSerGlnAsnGlyHsThr	640	
Db	1885	TATGACCTGTTGGCCATTGTCGCTGCTTCAATGTCAGATGTCAGTC	2004	
Qy	641	GluValLeuLeuAspAsnGlyAlaGlyAlaAspSerPheIleGluSerGlnAsnGlyHsThr	660	
Db	1945	GAAGTTGGAACTTTGGATAATGTCAGGCGTGTGTCAGGTC	2044	
Qy	661	TyrSerArgIlePheThrAlaIleThrGluAsnIleArgTyrsIleLeuVal	680	
Db	2005	TACTCAGGTATTTCAGGATAATGCTGAAATGAGCTATAAGGCGCT	2064	
Qy	681	HisGlyGlyAlaAsnThrAlaAsnGlyLeuAspLeuArgProProLeuAsnArgAlaAlaLys	700	
Db	2065	CATGGGAGAAACATGCGCTTAATAGGCCATTGCGCTTCACGCT	2124	
Qy	701	IlePheGlyIlePheValArgIleGlyIleGluAlaAsnProProArgProGluIleAsp	720	
Db	2125	ATACAGGTCGGTTAGTGAAGGAAATGAGGAAATGGCAAAAGCGCA	2184	
Qy	721	GluAspPheGlnThrIleLeuGluLysPheSerIleGlnThrAlaS19GlyAlaPheVal	740	
Db	2185	GGGGAACTCGACCCCTGGGATTCAAGCTCCGGAACTGGCTATTGCG	2244	
Qy	761	LeuAspAlaThrValIleIleSerIleLeuIleGluAsnSerProLysIleLeuAsp	780	
Db	2245	GTATCAGTCAGTCAGCTCCAGCTTCAGCTCAGCTCAGTCATCAG	2304	
Qy	781	PheAspPheGlyLysValGlnArgIleGlyIleLeuAspIleLeuAsp	800	
Db	2365	TCTGATGTTGGAAAGTCAAGTCAATCATCATGATAATGCTAATCT	2424	
Qy	801	ArgAspSerPheAspAspAlaIleGluGlnValAsnThrAspLeuSerProLysIleLeuAsp	820	
Db	2425	AGGAGCTTGTGATGCTGGCTTCAGTAACTGATGCTTCAATGAGGAA	2484	

